

Serial Number: 10/005,675

CRF Processing Date: 12/29/2001

Edited by: AN

Verified by: AN

(STIC stat

ENTERED

#4

☐

Changed a file from non-ASCII to ASCII

☐

Changed the margins in cases where the sequence text was "wrapped" down to the next line.

☐

Edited a format error in the Current Application Data section, specifically:

☐

Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____

☐

Added the mandatory heading and subheadings for "Current Application Data".

☐

Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.

☐

Changed the spelling of a mandatory field (the headings or subheadings), specifically:

☐

Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were:

☐

Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

☐

Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.

☐

Inserted colons after headings/subheadings. Headings edited included:

☐

Deleted extra, invalid, headings used by an applicant, specifically:

☐

Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as _____

☐

Inserted mandatory headings, specifically:

☐

Corrected an obvious error in the response, specifically:

☐

Edited identifiers where upper case is used but lower case is required, or vice versa.

☐

Corrected an error in the Number of Sequences field, specifically:

☐

A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.

☐

Deleted ending stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected:

☒

Other:

deleted duplicate "Sequence Listing" at beginning of page 7

Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/005,675

DATE: 12/20/2001

TIME: 20:57:11

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF3\12202001\J005675.raw

SEQUENCE LISTING

4 (1) GENERAL INFORMATION:

6 (i) APPLICANT: Shak, Steven

8 (ii) TITLE OF INVENTION: Anti-Infective Therapy

10 (iii) NUMBER OF SEQUENCES: 25

12 (iv) CORRESPONDENCE ADDRESS:

13 (A) ADDRESSEE: Genentech, Inc.

14 (B) STREET: 1 DNA Way

15 (C) CITY: South San Francisco

16 (D) STATE: California

17 (E) COUNTRY: USA

18 (F) ZIP: 94080

20 (v) COMPUTER READABLE FORM:

21 (A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

22 (B) COMPUTER: IBM PC compatible

23 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

24 (D) SOFTWARE: WinPatin (Genentech)

26 (vi) CURRENT APPLICATION DATA:

C--> 27 (A) APPLICATION NUMBER: US/10/005,675

C--> 28 (B) FILING DATE: 07-Nov-2001

29 (C) CLASSIFICATION:

59 (vii) PRIOR APPLICATION DATA:

32 (A) APPLICATION NUMBER: 09/669306

33 (B) FILING DATE: 25-Sep-2001

36 (A) APPLICATION NUMBER: 08/873506

37 (B) FILING DATE: 08-Dec-1999

40 (A) APPLICATION NUMBER: 08/643195

41 (B) FILING DATE: 06-May-1996

44 (A) APPLICATION NUMBER: 08/459909

45 (B) FILING DATE: 02-Jun-1995

48 (A) APPLICATION NUMBER: 08/191749

49 (B) FILING DATE: 03-Feb-1994

52 (A) APPLICATION NUMBER: 07/914,226

53 (B) FILING DATE: 13-Jul-1992

56 (A) APPLICATION NUMBER: 07/448038

57 (B) FILING DATE: 08-Dec-1989

60 (A) APPLICATION NUMBER: 07/289958

61 (B) FILING DATE: 23-Dec-1988

63 (viii) ATTORNEY/AGENT INFORMATION:

64 (A) NAME: Johnston, Sean A.

65 (B) REGISTRATION NUMBER: 35,910

66 (C) REFERENCE/DOCKET NUMBER: P0530P1C10

68 (ix) TELECOMMUNICATION INFORMATION:

69 (A) TELEPHONE: 650/225-3562

70 (B) TELEFAX: 650/952-9881

71 (2) INFORMATION FOR SEQ ID NO: 1:

73 (i) SEQUENCE CHARACTERISTICS:

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/005,675

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Input Set : A:\PTO.AMC.txt

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```

74      (A) LENGTH: 51 base pairs
75      (B) TYPE: Nucleic Acid
76      (C) STRANDEDNESS: Single
77      (D) TOPOLOGY: Linear
79      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
82  GTGCTGGACA CCTACCAGTA TGATGATGGC TGTGAGTCCT GTGGCAATGA 50
84  C 51
86  (2) INFORMATION FOR SEQ ID NO: 2:
88      (i) SEQUENCE CHARACTERISTICS:
89          (A) LENGTH: 17 amino acids
90          (B) TYPE: Amino Acid
91          (D) TOPOLOGY: Linear
93      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
95  Val Leu Asp Thr Tyr Gln Tyr Asp Asp Gly Cys Glu Ser Cys Gly
96    1             5             10             15
98  Asn Asp
101  (2) INFORMATION FOR SEQ ID NO: 3:
103      (i) SEQUENCE CHARACTERISTICS:
104          (A) LENGTH: 71 base pairs
105          (B) TYPE: Nucleic Acid
106          (C) STRANDEDNESS: Single
107          (D) TOPOLOGY: Linear
109      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
112  TATGACGTCT ACCTGGACGT GCAGCAGAAG TGGCATCTGA ATGATGTGAT 50
114  GCTGATGGGC GACTTCAACG C 71
116  (2) INFORMATION FOR SEQ ID NO: 4:
118      (i) SEQUENCE CHARACTERISTICS:
119          (A) LENGTH: 23 amino acids
120          (B) TYPE: Amino Acid
121          (D) TOPOLOGY: Linear
123      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
125  Tyr Asp Val Tyr Leu Asp Val Gln Gln Lys Trp His Leu Asn Asp
126    1             5             10             15
128  Val Met Leu Met Gly Asp Phe Asn
129             20
131  (2) INFORMATION FOR SEQ ID NO: 5:
133      (i) SEQUENCE CHARACTERISTICS:
134          (A) LENGTH: 42 base pairs
135          (B) TYPE: Nucleic Acid
136          (C) STRANDEDNESS: Single
137          (D) TOPOLOGY: Linear
139      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
142  CTGAAGATCG CAGCCTTCAA CATCCAGACA TTTGGGGAGA CC 42
144  (2) INFORMATION FOR SEQ ID NO: 6:
146      (i) SEQUENCE CHARACTERISTICS:
147          (A) LENGTH: 42 base pairs
148          (B) TYPE: Nucleic Acid
149          (C) STRANDEDNESS: Single
150          (D) TOPOLOGY: Linear

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152 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
155 TCCGCATGTC CCAGGGCCAC AGGCAGCGTT TCCTGGTAGG AC 42
157 (2) INFORMATION FOR SEQ ID NO: 7:
159 (i) SEQUENCE CHARACTERISTICS:
160 (A) LENGTH: 31 base pairs
161 (B) TYPE: Nucleic Acid
162 (C) STRANDEDNESS: Single
163 (D) TOPOLOGY: Linear
165 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
168 TTGAAGATCG CAGCCTTCAA CATCCAGACA T 31
170 (2) INFORMATION FOR SEQ ID NO: 8:
172 (i) SEQUENCE CHARACTERISTICS:
173 (A) LENGTH: 31 base pairs
174 (B) TYPE: Nucleic Acid
175 (C) STRANDEDNESS: Single
176 (D) TOPOLOGY: Linear
178 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
181 CTGGATGTTG AAGGVTGCGA TCTTCAATGC A 31
183 (2) INFORMATION FOR SEQ ID NO: 9:
185 (i) SEQUENCE CHARACTERISTICS:
186 (A) LENGTH: 42 base pairs
187 (B) TYPE: Nucleic Acid
188 (C) STRANDEDNESS: Single
189 (D) TOPOLOGY: Linear
191 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
194 CTAGAATTAT GTTAAAAATT GCAGCATTTA ATATTCAAAC AT 42
196 (2) INFORMATION FOR SEQ ID NO: 10:
198 (i) SEQUENCE CHARACTERISTICS:
199 (A) LENGTH: 34 base pairs
200 (B) TYPE: Nucleic Acid
201 (C) STRANDEDNESS: Single
202 (D) TOPOLOGY: Linear
204 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
207 TTGAATATTA AATGCTGCAA TTTTAAACAT AATT 34
209 (2) INFORMATION FOR SEQ ID NO: 11:
211 (i) SEQUENCE CHARACTERISTICS:
212 (A) LENGTH: 7 amino acids
213 (B) TYPE: Amino Acid
214 (D) TOPOLOGY: Linear
216 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:
218 Met Leu Lys Ile Ala Ala Phe
219 1 5
221 (2) INFORMATION FOR SEQ ID NO: 12:
223 (i) SEQUENCE CHARACTERISTICS:
224 (A) LENGTH: 1039 base pairs
225 (B) TYPE: Nucleic Acid
226 (C) STRANDEDNESS: Double
227 (D) TOPOLOGY: Linear
229 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

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232 TCCTGCACAG GCAGTGCCTT GAAGTGCTTC TTCAGAGACC TTTCTTCATA 50
234 GACTACTTTT TTTTCTTTAA GCAGCAAAAG GAGAAAATTG TCATCAAAGG 100
236 ATATTCCAGA TTCTTGACAG CATTCTCGTC ATCTCTGAGG ACATCACCAT 150
238 CATCTCAGGA TGAGGGGCAT GAAGCTGCTG GGGGCGCTGC TGGCACTGGC 200
240 GGCCCTACTG CAGGGGGCCG TGTCCCTGAA GATCGCAGCC TTCAACATCC 250
242 AGACATTTGG GGAGACCAAG ATGTCCAATG CCACCCTCGT CAGCTACATT 300
244 GTGCAGATCC TGAGCCGCTA TGACATCGCC CTGGTCCAGG AGGTCAGAGA 350
246 CAGCCACCTG ACTGCCGTGG GGAAGCTGCT GGACAACCTC AATCAGGATG 400
248 CACCAGACAC CTATCACTAC GTGGTCAGTG AGCCACTGGG ACGGAACAGC 450
250 TATAAGGAGC GCTACCTGTT CGTGTCAGG CCTGACCAGG TGTCTGCGGT 500
252 GGACAGCTAC TACTACGATG ATGGCTGCGA GCCCTGCGGG AACGACACCT 550
254 TCAACCGAGA GCCAGCCATT GTCAGGTTCT TCTCCCGGTT CACAGAGGTC 600
256 AGGGAGTTTG CCATTGTTCC CCTGCATGCG GCGGCGGGG ACGCAGTAGC 650
258 CGAGATCGAC GCTCTCTATG ACGTCTACCT GGATGTCCAA GAGAAATGGG 700
260 GCTTGGAGGA CGTCATGTTG ATGGGCGACT TCAATGCGGG CTGCAGCTAT 750
262 GTGAGACCCT CCCAGTGGTC ATCCATCCGC CTGTGGACAA GCGGACCTT 800
264 CCAGTGGCTG ATCCCCGACA GCGCTGACAC CACAGCTACA CCCACGCACT 850
266 GTGCCTATGA CAGGATCGTG GTTGTCAGGA TGCTGCTCCG AGGCGCCGTT 900
268 GTTCCCGACT CGGCTCTTCC CTTTAACTTC CAGGCTGCCT ATGGCCTGAG 950
270 TGACCAACTG GCCCAAGCCA TCAGTGACCA CTATCCAGTG GAGGTGATGC 1000
272 TGAAGTGAGC AGCCCCTCCC CACACCAAGT GAACTGCAG 1039

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(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 341 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

```

283 Ser Cys Thr Gly Ser Ala Leu Lys Cys Phe Phe Arg Asp Leu Ser
284 1 5 10 15
286 Ser Thr Thr Phe Phe Ser Leu Ser Ser Lys Arg Arg Lys Leu Ser
287 20 25 30
289 Ser Lys Asp Ile Pro Asp Ser Gln His Ser Arg His Leu Gly His
290 35 40 45
292 His His His Leu Arg Met Arg Gly Met Lys Leu Leu Gly Ala Leu
293 50 55 60
295 Leu Ala Leu Ala Ala Leu Leu Gln Gly Ala Val Ser Leu Lys Ile
296 65 70 75
298 Ala Ala Phe Asn Ile Gln Thr Phe Gly Glu Thr Lys Met Ser Asn
299 80 85 90
301 Ala Thr Leu Val Ser Tyr Ile Val Gln Ile Leu Ser Arg Tyr Asp
302 95 100 105
304 Ile Ala Leu Val Gln Glu Val Arg Asp Ser His Leu Thr Ala Val
305 110 115 120
307 Gly Lys Leu Leu Asp Asn Leu Asn Gln Asp Ala Pro Asp Thr Tyr
308 125 130 135
310 His Tyr Val Val Ser Glu Pro Leu Gly Arg Asn Ser Tyr Lys Glu
311 140 145 150
313 Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val Ser Ala Val Asp
314 155 160 165

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```

316 Ser Tyr Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn Asp Thr
317                               170                               175                               180
319 Phe Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe Thr
320                               185                               190                               195
322 Glu Val Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly
323                               200                               205                               210
325 Asp Ala Val Ala Glu Ile Asp Ala Leu Tyr Asp Val Tyr Leu Asp
326                               215                               220                               225
328 Val Gln Glu Lys Trp Gly Leu Glu Asp Val Met Leu Met Gly Asp
329                               230                               235                               240
331 Phe Asn Ala Gly Cys Ser Tyr Val Arg Pro Ser Gln Trp Ser Ser
332                               245                               250                               255
334 Ile Arg Leu Trp Thr Ser Pro Thr Phe Gln Trp Leu Ile Pro Asp
335                               260                               265                               270
337 Ser Ala Asp Thr Thr Ala Thr Pro Thr His Cys Ala Tyr Asp Arg
338                               275                               280                               285
340 Ile Val Val Ala Gly Met Leu Leu Arg Gly Ala Val Val Pro Asp
341                               290                               295                               300
343 Ser Ala Leu Pro Phe Asn Phe Gln Ala Ala Tyr Gly Leu Ser Asp
344                               305                               310                               315
346 Gln Leu Ala Gln Ala Ile Ser Asp His Tyr Pro Val Glu Val Met
347                               320                               325                               330
349 Leu Lys Ala Ala Pro Pro His Thr Ser Thr Ala
350                               335                               340
352 (2) INFORMATION FOR SEQ ID NO: 14:
354   (i) SEQUENCE CHARACTERISTICS:
355       (A) LENGTH: 260 amino acids
356       (B) TYPE: Amino Acid
357       (D) TOPOLOGY: Linear
359   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:
361 Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr Phe Gly Glu Thr Lys
362   1           5           10           15
364 Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val Gln Ile Leu Ser
365           20           25           30
367 Arg Tyr Asp Ile Ala Leu Val Gln Glu Val Arg Asp Ser His Leu
368           35           40           45
370 Thr Ala Val Gly Lys Leu Leu Asp Asn Leu Asn Gln Asp Ala Pro
371           50           55           60
373 Asp Thr Tyr His Tyr Val Val Ser Glu Pro Leu Gly Arg Asn Ser
374           65           70           75
376 Tyr Lys Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val Ser
377           80           85           90
379 Ala Val Asp Ser Tyr Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly
380           95          100          105
382 Asn Asp Thr Phe Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser
383          110          115          120
385 Arg Phe Thr Glu Val Arg Glu Phe Ala Ile Val Pro Leu His Ala
386          125          130          135
388 Ala Pro Gly Asp Ala Val Ala Glu Ile Asp Ala Leu Tyr Asp Val

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/005,675

DATE: 12/20/2001

TIME: 20:57:12

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF3\12202001\J005675.raw

L:27 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:28 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]